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humanVR1 gene with translation of open reading frame

Input file Fchrb87a6.seq; Output File Fchrb87a6.tra
Sequence length 3909

GTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAA
CGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGG
GCAGTGAGCGCAACGCACTTGC GG CAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGC
GCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACT
GCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTGCGGGCAGTG
AGCGCAACGCACTGCGGGCAGTGAGCGCAACGCACTTAATGTGAGTTAGCTCACTCATTAGGCACCCAGGCTTTACAC
TTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATT
ACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTC CGGGTCGACCC
ACGCGTCCGAAAACACACCTCTCTGCTGTGGAAGACTGTGCAATGGCACAGCCGAGAGCTTGGTTGGGAGGTTGAA
GTGCTCTGGGGAGAATTCTGTAGATCATCCTCAGAAAAGCCTTGCCCTGGTGTTCTACCAGAAAACGTCTCCCAATCAC
CCAGAAAAGCTGTCCACAGTAGTCCCCCTTATCCACGGGTGTCACTTTCCATGGGTTCAAGTTATTTGCGGTCAACCAC
GGTCTGCCAATATTAAATGGAAAATTCTTCAAACAGTTCCCAAGTTTCCCTTGTGCATTGTTCTGAGCAGTGTGATGA
AGAGTCTCTGCCGTGCCATCTGGGATGCAAACCGTCCCTGTGTCCCCACGTCCAGGCCGTAGATGCTCCCCGCCGGTC
AGTCACTTAGTCGTGATCGCCCGTCTGGTATCACAGTGCTTCTGTTCAAGTTGCACACTGGGCCACAGAGGATCCA

M	K	K	W	S	S	T	D	L	G	T	A	A	D	P	L	Q	K	18		
GCAAGG	ATG	AAG	AAA	TGG	AGC	AGC	ACA	GAC	TTG	GGG	ACA	GCT	GCG	GAC	CCA	CTC	CAA	AAG	54	
D	T	C	P	D	P	L	D	G	D	P	N	S	R	P	P	P	A	K	P	38
GAC	ACC	TGC	CCA	GAC	CCC	CTG	GAT	GGA	GAC	CCT	AAC	TCC	AGG	CCA	CCT	CCA	GCC	AAG	CCC	114
Q	L	P	T	A	K	S	R	T	R	L	F	G	K	G	D	S	E	E	A	58
CAG	CTC	CCC	ACG	GCC	AAG	AGC	CGC	ACC	CGG	CTC	TTT	GGG	AAG	GGT	GAC	TCG	GAG	GAG	GCT	174
F	P	V	D	C	P	H	E	E	G	E	L	D	S	C	P	T	I	T	V	78
TTC	CCG	GTG	GAT	TGC	CCC	CAC	GAG	GAA	GGT	GAG	TTG	GAC	TCC	TGC	CCG	ACC	ATC	ACA	GTC	234
S	P	V	I	T	I	Q	R	P	G	D	G	P	T	G	A	R	L	L	S	98
AGC	CCT	GTT	ATC	ACC	ATC	CAG	AGG	CCA	GGA	GAC	GGC	CCC	ACC	GGT	GCC	AGG	CTG	CTG	TCC	294

Fig. 1A

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Q D S V A A S T E K T L R L Y D R R S I 118
CAG GAC TCT GTC GCC GCC AGC ACC GAG AAG ACC CTC AGG CTC TAT GAT CGC AGG AGT ATC 354

F E A V A Q N N C Q D L E S L L L F L Q 138
TTT GAA GCC GTT GCT CAG AAT AAC TGC CAG GAT CTG GAG AGC CTG CTG CTC TTC CTG CAG 414

K S K K H L T D N E F K D P E T G K T C 158
AAG AGC AAG AAG CAC CTC ACA GAC AAC GAG TTC AAA GAC CCT GAG ACA GGG AAG ACC TGT 474

L L K A M L N L H D G Q N T T I P L L L 178
CTG CTG AAA GCC ATG CTC AAC CTG CAC GAC GGA CAG AAC ACC ACC ATC CCC CTG CTC CTG 534

E I A R Q T D S L K E L V N A S Y T D S 198
GAG ATC GCG CGG CAA ACG GAC AGC CTG AAG GAG CTT GTC AAC GCC AGC TAC ACG GAC AGC 594

Y Y K G Q T A L H I A I E R R N M A L V 218
TAC TAC AAG GGC CAG ACA GCA CTG CAC ATC GCC ATC GAG AGA CGC AAC ATG GCC CTG GTG 654

T L L V E N G A D V Q A A A H G D F F K 238
ACC CTC CTG GTG GAG AAC GGA GCA GAC GTC CAG GCT GCG GCC CAT GGG GAC TTC TTT AAG 714

K T K G R P G F Y F G E L P L S L A A C 258
AAA ACC AAA GGG CGG CCT GGA TTC TAC TTC GGT GAA CTG CCC CTG TCC CTG GCC GCG TGC 774

T N Q L G I V K F L L Q N S W Q T A D I 278
ACC AAC CAG CTG GGC ATC GTG AAG TTC CTG CTG CAG AAC TCC TGG CAG ACG GCC GAC ATC 834

S A R D S V G N T V L H A L V E V A D N 298
AGC GCC AGG GAC TCG GTG GGC AAC ACG GTG CTG CAC GCC CTG GTG GAG GTG GCC GAC AAC 894

T A D N T K F V T S M Y N E I L M L G A 318
ACG GCC GAC AAC ACG AAG TTT GTG ACG AGC ATG TAC AAT GAG ATT CTG ATG CTG GGG GCC 954

K L H P T L K L E E L T N K K G M T P L 338
AAA CTG CAC CCG ACG CTG AAG CTG GAG GAG CTC ACC AAC AAG AAG GGA ATG ACG CCG CTG 1014

A L A A G T G K I G V L A Y I L Q R E I 358
GCT CTG GCA GCT GGG ACC GGG AAG ATC GGG GTC TTG GCC TAT ATT CTC CAG CGG GAG ATC 1074

Q E P E C R H L S R K F T E W A Y G P V 378
CAG GAG CCC GAG TGC AGG CAC CTG TCC AGG AAG TTC ACC GAG TGG GCC TAC GGG CCC GTG 1134

H S S L Y D L S C I D T C E K N S V L E 398
CAC TCC TCG CTG TAC GAC CTG TCC TGC ATC GAC ACC TGC GAG AAG AAC TCG GTG CTG GAG 1194

V I A Y S S S E T P N R H D M L L V E P 418
GTG ATC GCC TAC AGC AGC AGC GAG ACC CCT AAT CGC CAC GAC ATG CTC TTG GTG GAG CCG 1254

Fig. 1B

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L N R L L Q D K W D R F V K R I F Y F N 438
CTG AAC CGA CTC CTG CAG GAC AAG TGG GAC AGA TTC GTC AAG CGC ATC TTC TAC TTC AAC 1314

F L V Y C L Y M I I F T M A A Y Y R P V 458
TTC CTG GTC TAC TGC CTG TAC ATG ATC ATC TTC ACC ATG GCT GCC TAC TAC AGG CCC GTG 1374

D G L P P F K M E K I G D Y F R V T G E 478
GAT GGC TTG CCT CCC TTT AAG ATG GAA ARA ATT GGA GAC TAT TTC CGA GTT ACT GGA GAG 1434

I L S V L G G V Y F F F R G I Q Y F L Q 498
ATC CTG TCT GTG TTA GGA GGA GTC TAC TTC TTT TTC CGA GGG ATT CAG TAT TTC CTG CAG 1494

R R P S M K T L F V D S Y S E M L F F L 518
AGG CGG CCG TCG ATG AAG ACC CTG TTT GTG GAC AGC TAC AGT GAG ATG CTT TTC TTT CTG 1554

Q S L F M L A T V V L Y F S H L K E Y V 538
CAG TCA CTG TTC ATG CTG GCC ACC GTG GTG CTG TAC TTC AGC CAC CTC AAG GAG TAT GTG 1614

A S M V F S L A L G W T N M L Y Y T R G 558
GCT TCC ATG GTA TTC TCC CTG GCC TTG GGC TGG ACC AAC ATG CTC TAC TAC ACC CGC GGT 1674

F Q Q M G I Y A V M I E K M I L R D L C 578
TTC CAG CAG ATG GGC ATC TAT GCC GTC ATG ATA GAG AAG ATG ATC CTG AGA GAC CTG TGC 1734

R F M F V Y I V F L F G F S T A V V T L 598
CGT TTC ATG TTT GTC TAC ATC GTC TTC TTG TTC GGG TTT TCC ACA GCG GTG GTG ACG CTG 1794

I E D G K N D S L P S E S T S H R W R G 618
ATT GAA GAC GGG AAG AAT GAC TCC CTG CCG TCT GAG TCC ACG TCG CAC AGG TGG CGG GGG 1854

P A C R P P D S S Y N S L Y S T C L E L 638
CCT GCC TGC AGG CCC CCC GAT AGC TCC TAC AAC AGC CTG TAC TCC ACC TGC CTG GAG CTG 1914

F K F T I G M G D L E F T E N Y D F K A 658
TTC AAG TTC ACC ATC GGC ATG GGC GAC CTG GAG TTC ACT GAG AAC TAT GAC TTC AAG GCT 1974

V F I I L L L A Y V I L T Y I L L L N M 678
GTC TTC ATC ATC CTG CTG CTG GCC TAT GTA ATT CTC ACC TAC ATC CTC CTG CTC AAC ATG 2034

L I A L M G E T V N K I A Q E S K N I W 698
CTC ATC GCC CTC ATG GGT GAG ACT GTC AAC AAG ATC GCA CAG GAG AGC AAG AAC ATC TGG 2094

K L Q R A I T I L D T E K S F L K C M R 718
AAG CTG CAG AGA GCC ATC ACC ATC CTG GAC ACG GAG AAG AGC TTC CTT AAG TGC ATG AGG 2154
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Fig. 1C

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K  A  F  R  S  G  K  L  L  Q  V  G  Y  T  P  D  G  K  D  D  738
AAG GCC TTC CGC TCA GGC AAG CTG CTG CAG GTG GGG TAC ACA CCT GAT GGC AAG GAC GAC 2214

Y  R  W  C  F  R  V  D  E  V  N  W  T  T  W  N  T  N  V  G  758
TAC CGG TGG TGC TTC AGG GTG GAC GAG GTG AAC TGG ACC ACC TGG AAC ACC AAC GTG GGC 2274

I  I  N  E  D  P  G  N  C  E  G  V  K  R  T  L  S  F  S  L  778
ATC ATC AAC GAA GAC CCG GGC AAC TGT GAG GGC GTC AAG CGC ACC CTG AGC TTC TCC CTG 2334

R  S  S  R  V  S  G  R  H  W  K  N  F  A  L  V  P  L  L  R  798
CGG TCA AGC AGA GTT TCA GGC AGA CAC TGG AAG AAC TTT GCC CTG GTC CCC CTT TTA AGA 2394

E  A  S  A  R  D  R  Q  S  A  Q  P  E  E  V  Y  L  R  Q  F  818
GAG GCA AGT GCT CGA GAT AGG CAG TCT GCT CAG CCC GAG GAA GTT TAT CTG CGA CAG TTT 2454

S  G  S  L  K  P  E  D  A  E  V  F  K  S  P  A  A  S  G  E  838
TCA GGG TCT CTG AAG CCA GAG GAC GCT GAG GTC TTC AAG AGT CCT GCC GCT TCC GGG GAG 2514

K  *
AAG TGA 840
2520
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GGACGTCACGCAGACAGCACTGTCAACACTGGGCCTTAGGAGACCCCGTTGCCACGGGGGGCTGCTGAGGGAACACCAG
TGCTCTGTCAGCAGCCTGGCCTGGTCTGTGCCTGCCCAGCATGTTCCCAAATCTGTGCTGGACAAGCTGTGGGAAGCGT
TCTTGGAAGCATGGGGAGTGATGTACATCCAACCGTCACTGTCCCCAAGTGAATCTCCTAACAGACTTTCAGGTTTTTA
CTCACTTTACTAAAAAAAAAAAAAAAAAGGGCGGCCGCTTA
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Fig. 1D

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Full-length human VR2

Input file Flh21e11.seq; Output File Flh21e11.tra
Sequence length 2809

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GGCTAGCCTGTCCTGACAGGGGAGAGTTAAGCTCCCGTTCTCCACCGTGCCGGCTGGCCAGGTGGGCTGAGGGTGACCG
AGAGACCAGAACCTGCTTGCTGGAGCTTAGTGCTCAGAGCTGGGGAGGGAGGTTCCGCCGCTCCTCTGCTGTCAGCGCC
GGCAGCCCCTCCCGGCTTCACTTCCTCCCGCAGCCCCTGCTACTGAGAAGCTCCGGGATCCCAGCAGCCGCCACGCCCT
GGCCTCAGCCTGCGGGGCTCCAGTCAGGCCAACACCGACGCGCAGCTGGGAGGAAGACAGGACCCTTGACATCTCCATC

                                     M   T   S   P   S   S   S   P           8
TGCACAGAGGTCCTGGCTGGACCGAGCAGCCTCCTCCTCTAGG ATG ACC TCA CCC TCC AGC TCT CCA      24

V   F   R   L   E   T   L   D   G   G   Q   E   D   G   S   E   A   D   R   G      28
GTT TTC AGG TTG GAG ACA TTA GAT GGA GGC CAA GAA GAT GGC TCT GAG GCG GAC AGA GGA      84

K   L   D   F   G   S   G   L   P   P   M   E   S   Q   F   Q   G   E   D   R      48
AAG CTG GAT TTT GGG AGC GGG CTG CCT CCC ATG GAG TCA CAG TTC CAG GGC GAG GAC CGG      144

K   F   A   P   Q   I   R   V   N   L   N   Y   R   K   G   T   G   A   S   Q      68
AAA TTC GCC CCT CAG ATA AGA GTC AAC CTC AAC TAC CGA AAG GGA ACA GGT GCC AGT CAG      204

P   D   P   N   R   F   D   R   D   R   L   F   N   A   V   S   R   G   V   P      88
CCG GAT CCA AAC CGA TTT GAC CGA GAT CGG CTC TTC AAT GCG GTC TCC CGG GST GTC CCC      264

E   D   L   A   G   L   P   E   Y   L   S   R   T   S   R   Y   L   T   D   S      108
GAG GAT CTG GCT GGA CTT CCA GAG TAC CTG AGC AAG ACC AGC AAG TAC CTC ACC GAC TCG      324

E   Y   T   E   G   S   T   G   K   T   C   L   M   K   A   V   L   N   L   K      128
GAA TAC ACA GAG GGC TCC ACA GGT AAG ACG TGC CTG ATG AAG GCT GTG CTG AAC CTT AAG      384

D   G   V   N   A   C   I   L   P   L   L   Q   I   D   R   D   S   G   N   P      148
GAC GGA GTC AAT GCC TGC ATT CTG CCA CTG CTG CAG ATC GAC AGG GAC TCT GGC AAT CCT      444

Q   P   L   V   N   A   Q   C   T   D   D   Y   Y   R   G   H   S   A   L   H      168
CAG CCC CTG GTA AAT GCC CAG TGC ACA GAT GAC TAT TAC CGA GGC CAC AGC GCT CTG CAC      504

I   A   I   E   K   R   S   L   Q   C   V   K   L   L   V   E   N   G   A   N      188
ATC GCC ATT GAG AAG AGG AGT CTG CAG TGT GTG AAG CTC CTG GTG GAG AAT GGG GCC AAT      564

V   H   A   R   A   C   G   R   F   F   Q   K   G   Q   G   T   C   F   Y   F      208
GTG CAT GCC CGG GCC TGC GGC CGC TTC TTC CAG AAG GGC CAA GGG ACT TGC TTT TAT TTC      624

G   E   L   P   L   S   L   A   A   C   T   K   Q   W   D   V   V   S   Y   L      228
GGT GAG CTA CCC CTC TCT TTG GCC GCT TGC ACC AAG CAG TGG GAT GTG GTA AGC TAC CTC      684
```

Fig. 2A

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L	E	N	P	H	Q	P	A	S	L	Q	A	T	D	S	Q	G	N	T	V	248
CTG	GAG	AAC	CCA	CAC	CAG	CCC	GCC	AGC	CTG	CAG	GCC	ACT	GAC	TCC	CAG	GGC	AAC	ACA	GTC	744
L	H	A	L	V	M	I	S	D	N	S	A	E	N	I	A	L	V	T	S	268
CTG	CAT	GCC	CTA	GTG	ATG	ATC	TCG	GAC	AAC	TCA	GCT	GAG	AAC	ATT	GCA	CTG	GTG	ACC	ACC	804
M	Y	D	G	L	L	Q	A	G	A	R	L	C	P	T	V	Q	L	E	D	288
ATG	TAT	GAT	GGG	CTC	CTC	CAA	GCT	GGG	GCC	CGC	CTC	TGC	CCT	ACC	GTG	CAG	CTT	GAG	GAC	864
I	R	N	L	Q	D	L	T	P	L	K	L	A	A	K	E	G	K	I	E	308
ATC	GCC	AAC	CTG	CAG	GAT	CTC	ACG	CCT	CTG	AAG	CTG	GCC	GCC	AAG	GAG	GGC	AAG	ATC	GAG	924
I	F	R	H	I	L	Q	R	E	F	S	G	L	S	H	L	S	R	K	F	328
ATT	TTC	AGG	CAC	ATC	CTG	CAG	CGG	GAG	TTT	TCA	GGA	CTG	AGC	CAC	CTT	TCC	CGA	AAG	TTC	984
T	E	W	C	Y	G	P	V	R	V	S	L	Y	D	L	A	S	V	D	S	348
ACC	GAG	TGG	TGC	TAT	GGG	CCT	GTC	CGG	GTG	TCG	CTG	TAT	GAC	CTG	GCT	TCT	GTG	GAC	AGC	1044
C	E	E	N	S	V	L	E	I	I	A	F	H	C	K	S	P	H	R	H	368
TGT	GAG	GAG	AAC	TCA	GTG	CTG	GAG	ATC	ATT	GCC	TTT	CAT	TGC	AAG	AGC	CCG	CAC	CGA	CAC	1104
R	M	V	V	L	E	P	L	N	K	L	L	Q	A	K	W	D	L	L	I	388
CGA	ATG	GTC	GTT	TTG	GAG	CCC	CTG	AAC	AAA	CTG	CTG	CAG	GCG	AAA	TGG	GAT	CTG	CTC	ATC	1164
P	K	F	F	L	N	F	L	C	N	L	I	Y	M	F	I	F	T	A	V	408
CCC	AAG	TTC	TTC	TTA	AAC	TTC	CTG	TGT	AAT	CTG	ATC	TAC	ATG	TTC	ATC	TTC	ACC	GCT	GTT	1224
A	Y	H	Q	P	T	L	K	K	Q	A	A	P	H	L	K	A	E	V	G	428
GCC	TAC	CAT	CAG	CCT	ACC	CTG	AAG	AAG	CAG	GCC	GCC	CCT	CAC	CTG	AAA	GCG	GAG	GTT	GGA	1284
N	S	M	L	L	T	G	H	I	L	I	L	L	G	G	I	Y	L	L	V	448
AAC	TCC	ATG	CTG	CTG	ACG	GGC	CAC	ATC	CTT	ATC	CTG	CTA	GGG	GGG	ATC	TAC	CTC	CTC	GTG	1344
G	Q	L	W	Y	F	W	R	R	H	V	F	I	W	I	S	F	I	D	S	468
GGC	CAG	CTG	TGG	TAC	TTC	TGG	CGG	CGC	CAC	GTG	TTC	ATC	TGG	ATC	TCG	TTC	ATA	GAC	AGC	1404
Y	F	E	I	L	F	L	F	Q	A	L	L	T	V	V	S	Q	V	L	C	488
TAC	TTT	GAA	ATC	CTC	TTC	CTG	TTC	CAG	GCC	CTG	CTC	ACA	GTG	GTG	TCC	CAG	GTG	CTG	TGT	1464
F	L	A	I	E	W	Y	L	P	L	L	V	S	A	L	V	L	G	W	L	508
TTC	CTG	GCC	ATC	GAG	TGG	TAC	CTG	CCC	CTG	CTT	GTG	TCT	GCG	CTG	GTG	CTG	GGC	TGG	CTG	1524
N	L	L	Y	Y	T	R	G	F	Q	H	T	G	I	Y	S	V	M	I	Q	528
AAC	CTG	CTT	TAC	TAT	ACA	CGT	GGC	TTC	CAG	CAC	ACA	GGC	ATC	TAC	AGT	GTC	ATG	ATC	CAG	1584

Fig. 2B

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K V I L R D L L R F L L I Y L V F L F G 548
AAG GTC ATC CTG CGG GAC CTG CTG CGC TTC CTT CTG ATC TAC TTA GTC TTC CTT TTC GGC 1644

F A V A L V S L S Q E A W R P E A P T G 568
TTC GCT GTA GCC CTG GTG AGC CTG AGC CAG GAG GCT TGG CGC CCC GAA GCT CCT ACA GGC 1704

P N A T E S V Q P M E G Q E D E G N G A 588
CCC AAT GCC ACA GAG TCA GTG CAG CCC ATG GAG GGA CAG GAG GAC GAG GGC AAC GGG GCC 1764

Q Y R G I L E A S L E L F K F T I G M G 608
CAG TAC AGG GGT ATC CTG GAA GCC TCC TTG GAG CTC TTC AAA TTC ACC ATC GGC ATG GGC 1824

E L A F Q E Q L H F R G M V L L L L L A 628
GAG CTG GCC TTC CAG GAG CAG CTG CAC TTC CGC GGC ATG GTG CTG CTG CTG CTG GGC 1884

Y V L L T Y I L L L N M L I A L M S E T 648
TAC GTG CTG CTC ACC TAC ATC CTG CTG CTC AAC ATG CTC ATC GCC CTC ATG AGC GAG ACC 1944

V N S V A T D S W S I W K L Q K A I S V 668
GTC AAC AGT GTC GCC ACT GAC AGC TGG AGC ATC TGG AAG CTG CAG AAA GCC ATC TCT GTC 2004

L E M E N G Y W W C R K K Q R A G V M L 688
CTG GAG ATG GAG AAT GGC TAT TGG TGG TGC AGG AAG AAG CAG CGG GCA GGT GTG ATG CTG 2064

T V G T K P D G S P D E R W C F R V E E 708
ACC GTT GGC ACT AAG CCA GAT GGC AGC CCG GAT GAG CGC TGG TGC TTC AGG GTG GAG GAG 2124

V N W A S W E Q T L P T L C E D P S G A 728
GTG AAC TGG GCT TCA TGG GAG CAG ACG CTG CCT ACG CTG TGT GAG GAC CCG TCA GGG GCA 2184

G V P R T L E N P V L A S P P K E D E D 748
GGT GTC CCT CGA ACT CTC GAG AAC CCT GTC CTG GCT TCC CCT CCC AAG GAG GAT GAG GAT 2244

G A S E E N Y V P V Q L L Q S N * 765
GGT GCC TCT GAG GAA AAC TAT GTG CCC GTC CAG CTC CTC CAG TCC AAC TGA 2295

TGGCCCAGATGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAACCACATCTGCTGGCTCTGGGGTCCCAGTG

AATTCTGGTGGCAAATATATATATTTTCACTAACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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Fig. 2C

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Partial human VR2 alternate form

Input file frhob12c4.seg; Output File frhob12c4.tra
Sequence length 1489

G	R	F	F	Q	K	G	Q	G	T	C	F	Y	F	G	E	L	P	L	19	
GC	GGC	CGC	TTC	TTC	CAG	AAG	GGC	CAA	GGG	ACT	TGC	TTT	TAT	TTC	GGT	GAG	CTA	CCC	CTC	57
S	L	A	A	C	T	K	Q	W	D	V	V	S	Y	L	L	E	N	P	H	39
TCT	TTG	GCC	GCT	TGC	ACC	AAG	CAG	TGG	GAT	GTG	GTA	AGC	TAC	CTC	CTG	GAG	AAC	CCA	CAC	117
Q	P	A	S	L	Q	A	T	D	S	Q	G	N	T	V	L	H	A	L	V	59
CAG	CCC	GCC	AGC	CTG	CAG	GCC	ACT	GAC	TCC	CAG	GGC	AAC	ACA	GTC	CTG	CAT	GCC	CTA	GTG	177
M	I	S	D	N	S	A	E	N	I	A	L	V	T	S	M	Y	D	G	L	79
ATG	ATC	TCG	GAC	AAC	TCA	GCT	GAG	AAC	ATT	GCA	CTG	GTG	ACC	AGC	ATG	TAT	GAT	GGG	CTC	237
L	Q	A	G	A	R	L	C	P	T	V	Q	L	E	D	I	R	N	L	Q	99
CTC	CAA	GCT	GGG	GCC	CGC	CTC	TGC	CCT	ACC	GTG	CAG	CTT	GAG	GAC	ATC	CGC	AAC	CTG	CAG	297
D	L	T	P	L	K	L	A	A	K	E	G	K	I	E	I	F	R	H	I	119
GAT	CTC	ACG	CCT	CTG	AAG	CTG	GCC	GCC	AAG	GAG	GGC	AAG	ATC	GAG	ATT	TTC	AGG	CAC	ATC	357
L	Q	R	E	F	S	G	L	S	H	L	S	R	K	F	T	E	W	C	Y	139
CTG	CAG	CGG	GAG	TTT	TCA	GGA	CTG	AGC	CAC	CTT	TCC	CGA	AAG	TTC	ACC	GAG	TGG	TGC	TAT	417
G	P	V	R	V	S	L	Y	D	L	A	S	V	D	S	C	E	E	N	S	159
GGG	CCT	GTC	CGG	GTG	TCG	CTG	TAT	GAC	CTG	GCT	TCT	GTG	GAC	AGC	TGT	GAG	GAG	AAC	TCA	477
V	L	E	I	I	A	F	H	C	K	S	P	H	R	H	R	M	V	V	L	179
GTG	CTG	GAG	ATC	ATT	GCC	TTT	CAT	TGC	AAG	AGC	CCG	CAC	CGA	CAC	CGA	ATG	GTC	GTT	TTG	537
E	P	L	N	K	L	L	Q	A	K	W	D	L	L	I	P	K	F	F	L	199
GAG	CCC	CTG	AAC	AAA	CTG	CTG	CAG	GCG	AAA	TGG	GAT	CTG	CTC	ATC	CCC	AAG	TTC	TTC	TTA	597
N	F	L	C	N	L	I	Y	M	F	I	F	T	A	V	A	Y	H	Q	P	219
AAC	TTC	CTG	TGT	AAT	CTG	ATC	TAC	ATG	TTC	ATC	TTC	ACC	GCT	GTT	GCC	TAC	CAT	CAG	CCT	657
T	L	K	K	Q	A	A	P	H	L	K	A	E	V	G	N	S	M	L	L	239
ACC	CTG	AAG	AAG	CAG	GCC	GCC	CCT	CAC	CTG	AAA	GCG	GAG	GTT	GGA	AAC	TCC	ATG	CTG	CTG	717
T	G	H	I	L	I	L	L	G	G	I	Y	L	L	V	G	Q	L	W	Y	259
ACG	GGC	CAC	ATC	CTT	ATC	CTG	CTA	GGG	GGG	ATC	TAC	CTC	CTC	GTG	GGC	CAG	CTG	TGG	TAC	777
F	W	R	R	H	V	F	I	W	I	S	F	I	D	S	Y	F	E	I	L	279
TTC	TGG	CGG	CGC	CAC	GTG	TTC	ATC	TGG	ATC	TCG	TTC	ATA	GAC	AGC	TAC	TTT	GAA	ATC	CTC	837

Fig. 3A

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```
F L F Q A L L T V V S Q V L C F L A I E 299
TTC CTG TTC CAG GCC CTG CTC ACA GTG GTG TCC CAG GTG CTG TGT TTC CTG GCC ATC GAG 897

W Y L P L L V S A L V L G W L N L L Y Y 319
TGG TAC CTG CCC CTG CTT GTG TCT GCG CTG GTG CTG GGC TGG CTG AAC CTG CTT TAC TAT 957

T R G F Q H T G I Y S V M I Q K K A I S 339
ACA CGT GGC TTC CAG CAC ACA GGC ATC TAC AGT GTC ATG ATC CAG AAG AAA GCC ATC TCT 1017

V L E M E N G Y W W C R K K Q R A G V M 359
GTC CTG GAG ATG GAG AAT GGC TAT TGG TGG TGC AGG AAG AAG CAG CGG GCA GGT GTG ATG 1077

L T V G T K P D G S P D E R W C F R V E 379
CTG ACC GTT GGC ACT AAG CCA GAT GGC AGC CCG GAT GAG CGC TGG TGC TTC AGG GTG GAG 1137

E V N W A S W E Q T L P T L C E D P S G 399
GAG GTG AAC TGG GCT TCA TGG GAG CAG ACG CTG CCT ACG CTG TGT GAG GAC CCG TCA GGG 1197

A G V P R T L E N P V L A S P P K E D E 419
GCA GGT GTC CCT CGA ACT CTC GAG AAC CCT GTC CTG GCT TCC CCT CCC AAG GAG GAT GAG 1257

D G A S E E N Y V P V Q L L Q S N * 437
GAT GGT GCC TCT GAG GAA AAC TAT GTG CCC GTC CAG CTC CTC CAG TCC AAC TGA 1311

TGGCCCAGATGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAACCACATCTGCTGGCTCTGGGGTCCCAGTG
AATTCTGGTGGCAAATATATATTTTCACTAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGA
CGGGACGCGTGGGTCGAC
```

Fig. 3B

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Partial rat VR2

Input file Flrxb147g11.seq; Output File Flrxb147g11.tra
Sequence length 1794

```
S T H A S A L S L A A C T K Q W D V V 19
G TCG ACC CAC GCG TCC GCT CTT TCT CTG GCT GCG TGC ACC AAG CAG TGG GAT GTG GTG 57

T Y L L E N P H Q P A S L E A T D S L G 39
ACC TAC CTC CTG GAG AAC CCA CAC CAG CCG GCC AGC CTG GAG GCC ACC GAC TCC CTG GGC 117

N T V L H A L V M I A D N S P E N S A L 59
AAC ACA GTC CTG CAT GCT CTG GTA ATG ATT GCA GAT AAC TCG CCT GAG AAC AGT GCC CTG 177

V I H M Y D G L L Q M G A R L C P T V Q 79
GTG ATC CAC ATG TAC GAC GGG CTT CTA CAA ATG GGG GCG CGC CTC TGC CCC ACT GTG CAG 237

L E E I S N H Q G L T P L K L A A K E G 99
CTT GAG GAA ATC TCC AAC CAC CAA GGC CTC ACA CCC CTG AAA CTA GCC GCC AAG GAA GGC 297

K I E I F R H I L Q R E F S G P Y Q P L 119
AAA ATC GAG ATT TTC AGG CAC ATT CTG CAG CGG GAA TTC TCA GGA CCG TAC CAG CCC CTT 357

S R K F T E W C Y G P V R V S L Y D L S 139
TCC CGA AAG TTT ACT GAG TGG TGT TAC GGT CCT GTG CGG GTA TCG CTG TAC GAC CTG TCC 417

S V D S W E K N S V L E I I A F H C K S 159
TCT GTG GAC AGC TGG GAA AAG AAC TCG GTG CTG GAG ATC ATC GCT TTT CAT TGC AAG AGC 477

P N R H R M V V L E P L N K L L Q E K W 179
CCG AAC CGG CAC CGC ATG GTG GTT TTA GAA CCA CTG AAC AAG CTT CTG CAG GAG AAA TGG 537

D R L V S R P F F N F A C Y L V Y M F I 199
GAT CGG CTC GTC TCA AGA TTC TTC TTC AAC TTC GCC TGC TAC TTG GTC TAC ATG TTC ATC 597

F T V V A Y H Q P S L D Q P A I P S S K 219
TTC ACC GTC GTT GCC TAC CAC CAG CCT TCC CTG GAT CAG CCA GCC ATC CCC TCA TCA AAA 657

A T F G E S M L L L G H I L I L L G G I 239
GCG ACT TTT GGG GAA TCC ATG CTG CTG CTG GGC CAC ATT CTG ATC CTG CTT GGG GGT ATT 717

Y L L L G Q L W Y F W R R R L F I W I S 259
TAC CTC TTA CTG GGC CAG CTG TGG TAC TTT TGG CGG CGG CGC CTG TTT ATC TGG ATC TCA 777

F M D S Y F E I L F L L Q A L L T V L S 279
TTC ATG GAC AGC TAC TTT GAA ATC CTC TTT CTC CTT CAG GCT CTG CTC ACA GTG CTG TCC 837
```

Fig. 4A

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Q V L R F M E T E W Y L P L L V L S L V	299
CAG GTG CTG CGC TTC ATG GAG ACT GAA TGG TAC CTA CCC CTG CTA GTG TTA TCC CTA GTG	897
L G W L N L L Y Y T R G F Q H T G I Y S	319
CTG GGC TGG CTG AAC CTG CTT TAC TAC ACA CGG GGC TTT CAG CAC ACA GGC ATC TAC AGT	957
V M I Q K V I L R D L L R F L L V Y L V	339
GTC ATG ATC CAG AAG GTC ATC CTT CGA GAC CTG CTC CGT TTC CTG CTG GTC TAC CTG GTC	1017
F L F G F A V A L V S L S R E A R S P K	359
TTC CTT TTC GGC TTT GCT GTA GCC CTA GTA AGC TTG AGC AGA GAG GCC CGA AGT CCC AAA	1077
A P E D N N S T V T E Q P T V G Q E E E	379
GCC CCT GAA GAT AAC AAC TCC ACA GTG ACG GAA CAG CCC ACG GTG GGC CAG GAG GAG GAG	1137
P A P Y R S I L D A S L E L F K F T I G	399
CCA GCT CCA TAT CGG AGC ATT CTG GAT GCC TCC CTA GAG CTG TTC AAG TTC ACC ATT GGT	1197
M G E L A F Q E Q L R F R G V V L L L L	419
ATG GGG GAG CTG GCT TTC CAG GAA CAG CTG CGT TTT CGT GGG GTG GTC CTG CTG TTG CTG	1257
L A Y V L L T Y V L L L N M L I A L M S	439
TTG GCC TAC GTC CTT CTC ACC TAC GTC CTG CTG CTC AAC ATG CTC ATT GCT CTC ATG AGC	1317
E T V N H V A D N S W S I W K L Q K A I	459
GAA ACT GTC AAC CAC GTT GCT GAC AAC AGC TGG AGC ATC TGG AAG TTG CAG AAA GCC ATC	1377
S V L E M E N G Y W W C R R K K H R E G	479
TCT GTC TTG GAG ATG GAG AAT GGT TAC TGG TGG TGC CGG AGG AAG AAA CAT CGT GAA GGG	1437
R L L K V G T R G D G T P D E R W C F R	499
AGG CTG CTG AAA GTC GGC ACC AGG GGG GAT GGT ACC CCT GAT GAG CGC TGG TGC TTC AGG	1497
V E E V N W A A W E K T L P T L S E D P	519
GTG GAG GAA GTA AAT TGG GCT GCT TGG GAG AAG ACT CTT CCC ACC TTA TCT GAG GAT CCA	1557
S G P G I T G N K K N P T S K P G K N S	539
TCA GGG CCA GGC ATC ACT GGT AAT AAA AAG AAC CCA ACC TCT AAA CCG GGG AAG AAC AGT	1617
A S E E D H L P L Q V L Q S P *	555
GCC TCA GAG GAA GAC CAT CTG CCC CTT CAG GTC CTC CAG TCC CCC TGA	1665
TGGCCCAGATGCAGCAGCAGGCTGGCAGGATGGAGTAGGGAATCTTCCCAGCCACACCAGAGGCTACTGAATTTTGGTG	
GAAATATAAATATTTTTTTTGCATAAAAAAAAAAAAAAGGGCGGCCGC	

Fig. 4B

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GAP of: humanvr2.pep check: 5746 from: 1 to: 764

humanVR2 Flh21e11

to: humanvr1.pep check: 6877 from: 1 to: 839

humanVR1_Fbh18547pat - fchrb87a6, 3909 bases, 4554 checksum.

Symbol comparison table:
/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1530 Length: 850
Ratio: 2.003 Gaps: 10
Percent Similarity: 55.378 Percent Identity: 46.348

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

humanvr2.pep x humanvr1.pep

```

1 .....MTSPSSSPVF 10
      |. | . .|
1 MKKWSSTD LGTAADPLQKDTCPDPLDGD P NSRPPPAKPQLPTAKSRTL F 50
      .
11 RLETL DGGQEDGSEADRGKLD FGSGLPPMESQFQGEDRKFAPQIRVNLNY 60
      : |. || : . : | |
51 GKGDSEEAFFVDCPHEEGEL DSCPTI.TVSPVITIQRPGDGPTGARLLSQ 99
      .
61 RKGTGASQPD PNRFD RDR LFN AVSRGVPE D LAGLPEYLSKTSKYLTDSEY 110
      ..: :|| :| ||.. :|| | :| |. |: |||. :
100 DSVAASTEKTLRLYDRRSIFEAVAQN NCQDLESLLLFLQSKKHLTDNEF 149
      .
111 TEGSTGKTCLMKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDY 160
      : |||||: ||. ||| || | ||:| | . . . |||| || |
150 KDPETGKTCLLKAMLNLHDGQNTTIP LLLLEIARQTDSLKELVNASYTDSY 199
      .
161 YRGHSALHIAIEKRS LQCVKLLVENGANVHARACGRFFQKGQG.TCFYFG 209
      |:| . |||||:|. : | |||||. | | | |||. | . | |||
200 YKGQTALHIAIERRNMALVTLLVENGADVQAAAHG DFFKKTGRPGFYFG 249

```

Fig. 5A

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```

210 ELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHALVMISDNS 259
    ||||| | : | : | : | | : | | ||||| : . ||
250 ELPLSLAACTNQLGIVKFLQNSWQTADISARDSVGNTVLHALVEVADNT 299

260 AENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAKEGKIEI 309
    | : | | | | . : | | : | | . . | : : | . : | | | | | :
300 ADNTKFVTSMYNEILMLGAKLHPTLKEELTNKKGMTPLALAAAGTGKIGV 349

310 FRHILQREFS..GLSHLSRKFTWECYGPVRVSLYDLASVDSCEENSVLEI 357
    : | | | | | | | | | | | | | | | | | | . : | . | . | | | :
350 LAYILQREIQEPECRHLSRKFTWAYGPVHSSLYDLSCIDTCEKNSVLEV 399

358 IAF.HCKSPHRHRMVVLEPLNKLQAKWDLIPK.FFLNFLCNLIYMFIF 405
    || : . . | . | | | . . | | | : | | | | : : | : | | : | | |
400 IAYSSSETPNRHDMLLVEPLNRLQDKWDRFVKRIFYFNFLVYCLYMIIF 449

406 TAVAYHQPTLKKQAAPHLKAEVGNMMLTGHILILLGGIYLLVGQLWYFW 455
    | | | : . | | . : | . . | | | . | | : | : | |
450 TMAAYYRPV..DGLPPFKMEKIGDYFRVTGEILSVLGGVYFFFRGIQYFL 497

456 RRHVFIWISFIDSYFEILFLFQALLTVVSQVLCFLAIEWYLPLLVSALVL 505
    . | : | | | | . | . | . | . | . | . | . | . | . |
498 QRRPSMKTLFVDSYSEMLFFLQSLFMLATVVLYFSHLKEYVASMVFSLAL 547

506 GWLNLLEYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGFAVALVS 555
    || : | | | | | | | | . | | : | . | | | | | | : : | : | | | | . | . |
548 GWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVYIVFLFGFSTAVVT 597

556 LSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLELFKFTI 605
    | : : . . | . | . | : | | | | | |
598 LIEDGKNDSLPSSESTSHRWGPACRPPD....SSYNSLYSTCLELFKFTI 643

606 GMGELAFQEQLHFRGMVLLLLLAYVLLTYILLNMLIALMSETVNSVATD 655
    ||| : | | | : . : : | | | | : | | | | | | | | | | | | | | : | :
644 GMGDLEFTENYDFKAVFIILLAYVILTYILLNMLIALMGETVNKIAQE 693

656 SWSIWKLQKAISVLEMENGYWWC.RKKQRAGVMLTVGTPDGSPDERWCF 704
    | . | | | | : | | . : | : | | | . | : | | | | | | | |
694 SKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGYPDGDGDDYRWCF 743

705 RVEEVNWASWEQTLPTLCEDPSGA.GVPRTLENPVLASPPKEDEDGASEE 753
    || : | | | | . | . : | | | | | | | . | | | |
744 RVDEVNWTWNTNVGIINEDPGNCEGVKRTLSFSLRSS....RVSGRHWK 789

754 NYVPVQLLQSN..... 764
    | : | | |
790 NFALVPLLREASARDRQSAQPEEVYLRQFSGSLKPEDA EVFKSPAASGEK 839

```

Fig. 5B

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GAP of: humanvr2.seq check: 8853 from: 1 to: 2809

humanVR2 21e11a, 2809 bases, 8853 checksum.

to: humanvr1.seq check: 4554 from: 1 to: 3909

humanVR1 Fbh18547pat - Import - complete

Symbol comparison table:
/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	14359	Length:	3934
Ratio:	5.112	Gaps:	15
Percent Similarity:	55.316	Percent Identity:	55.316

Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1

humanvr2.seq x humanvr1.seq

```

      .
      .
      .
1 .....GGCTAGCCTGTCCTGACAGGGGAGAG 26
      | | | | | | | |
801 TGTCCACAGTAGTCCCCCCTTATCCACGGGTGTCACCTTCCATGGGTTC 850
      .
      .
27 TTAAGCTCCCGTTCTCCACCGTGCCGGCTGGCCAGGTGGGCTGAGGGTGA 76
      | | | | | | | |
851 GTTATTTGCGGTCAACCACGGTCTGCCAATATTAAATGGAAAATTCTTCA 900
      .
      .
77 CCGAGAGACCAGAACCTGCTTGCTGGAGCTTAGTGCTCAGAGCTGGGGAG 126
      | | | | | | | |
901 AACAGTTCCCAAGTTTTCCCTTGTCATTGTTCTGAGCAGTGTGATGAAG 950
      .
      .
127 GGAGGTTCCGCCGCTCCTCTGCTGTCAGCGCCGGCAGCCCCTCCCGGCTT 176
      | | | | | | | |
951 AGTCTCTGCCGTGCCATCTGGGATGCAAACCGTCCCTGTGTCCCCCACGT 1000

```

Fig. 6A

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```

177 CACTTCCTCCCGCAGCCCCCTGCTACTGAGAAGCTCCGGGATCCCAGCAGC 226
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1001 CCAGGCCGTAGATGCTCCCCGCCGGTCAGTCACTTAGTCGTCAGATCGCC 1050

227 CGCCACGCCCTGGC.....CTCAGCCTGCGGG 253
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1051 CGTCCTGGTATCACAGTGCTTCTGTTCAGGTTGCACACTGGGCCACAGAG 1100

254 GCTCCAGTCAGGCCAACACCGACGCGCAGCTGGGAGGAAG..... 293
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1101 GATCCAGCAAGGATGAAGAAATGGAGCAGCACAGACTTGGGGACAGCTGC 1150

294 .....ACAGGACCCTTGACATCTCCATCTGCACAGAGGTCCTG 331
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1151 GGACCCACTCCAAAAGGACACCTGCCAGACCCCTGGATGGAGACCTA 1200

332 GCTGGACCGAGCAGCCTCCTCCTCCTAGGATGACCTCACCTCCAGC..T 379
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1201 ACTCCAGGCCACCTCCAGCCAAGCCCCAGCTCCCCACGGCCAAGAGCCGC 1250

380 CTCCAGTTTTTCAGGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCT 429
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1251 ACCCGGCTCTTTGGGAAGGGTGACTCGGAGGAGGCTTTCCCGGTGGATTG 1300

430 GAGGCGGACAGAGGAAAGCTGGATTTTGGGAGCGGGCTGCCTCCCATGGA 479
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1301 CCCCCACGAGGAAGGTGAGTTGGACTCCTGCCCGACCATCACAGTCAGCC 1350

480 GTCACAGTTCCAGGGCGAGGACCGGAAATTCGCCCCCTCAGATAAGAGTCA 529
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1351 CTGTTATCACCATCCAGAGGCCAGGAGACGGCCCCACCGGTGCCAGG..C 1398

530 ACCTCAACTACCGAAAGGGAACAGGTGCCAGTCAGCCGGATCCAAACCGA 579
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1399 TGCTGTCCCAGGACTCTGTCGCCGCCAGCACCGAGAAGACCTCAGGCTC 1448

580 TTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGAGGA 629
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1449 TATGATCGCAGGAGTATCTTTGAAGCCGTTGCTCAGAATAACTGCCAGGA 1498

630 TCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAGCAAGTACCTCACCG 679
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1499 TCTGGAGAGCCTGCTGCTCTTCCTGCAGAAGAGCAAGAAGCACCTCACAG 1548

```

Fig. 6B

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680 ACTCGGAATACACAGAGGGCTCCACAGGTAAGACGTGCCTGATGAAGGCT 729
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1549 ACAACGAGTTCAAAGACCCTGAGACAGGGAAGACCTGTCTGCTGAAAGCC 1598

730 GTGCTGAACCTTAAGGACGGAGTCAATGCCTGCATTCTGCCACTGCTGCA 779
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1599 ATGCTCAACCTGCACGACGGACAGAACACCACCATCCCCCTGCTCCTGGA 1648

780 GATCGACAGGGACTCTGGCAATCCTCAGCCCCTGGTAAATGCCCAGTGCA 829
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1649 GATCGCGCGGCAAACGGACAGCCTGAAGGAGCTTGTCAACGCCAGCTACA 1698

830 CAGATGACTATTACCGAGGCCACAGCGCTCTGCACATCGCCATTGAGAAG 879
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1699 CGGACAGCTACTACAAGGGCCAGACAGCACTGCACATCGCCATCGAGAGA 1748

880 AGGAGTCTGCAGTGTGTGAAGCTCCTGGTGGAGAATGGGGCCAATGTGCA 929
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1749 CGCAACATGGCCCTGGTGACCCTCCTGGTGGAGAACGGAGCAGACGTCCA 1798

930 TGCCCGGGCTGCGGCCGCTTCTTCCAGAAGGGCCAAG...GGACTTGCT 976
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1799 GGCTGCGGCCCATGGGGACTTCTTTAAGAAAACCAAAGGGCGGCCTGGAT 1848

977 TTTATTTTCGGTGAGCTACCCCTCTCTTTGGCCGCTTGACCAAGCAGTGG 1026
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1849 TCTACTTCGGTGAAGTGCACCTGTCCCTGGCCGCGTGACCAACCAGCTG 1898

1027 GATGTGGTAAGCTACCTCCTGGAGAACCCACACCAGCCCGCCAGCCTGCA 1076
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1899 GGCATCGTGAAGTTCCTGCTGCAGAACTCCTGGCAGACGGCCGACATCAG 1948

1077 GGCCACTGACTCCCAGGGCAACACAGTCCTGCATGCCCTAGTGATGATCT 1126
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1949 CGCCAGGGACTCGGTGGGCAACACGGTGCTGCACGCCCTGGTGGAGGTGG 1998

1127 CGGACAACTCAGCTGAGAACATTGCACTGGTGACCAGCATGTATGATGGG 1176
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
1999 CCGACAACACGGCCGACAACACGAAGTTTGTGACGAGCATGTACAATGAG 2048

1177 CTCCTCCAAGCTGGGGCCCGCCTCTGCCCTACCGTGCAGCTTGAGGACAT 1226
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
2049 ATTCTGATGCTGGGGGCCAAACTGCACCCGACGCTGAAGCTGGAGGAGCT 2098

```

Fig. 6C

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```
1227 CCGCAACCTGCAGGATCTCACGCCTCTGAAGCTGGCCGCCAAGGAGGGCA 1276
      | | | | | | | | | | | | | | | | | | | | | | | |
2099 CACCAACAAGAAGGGAATGACGCCGCTGGCTCTGGCAGCTGGGACCGGGA 2148
      .
1277 AGATCGAGATTTTCAGGCACATCCTGCAGCGGGAGTT.....TTCAGGA 1320
      | | | | | | | | | | | | | | | | | | | | | | | |
2149 AGATCGGGGTCTTGGCCTATATTCTCCAGCGGGAGATCCAGGAGCCCGAG 2198
      .
1321 CTGAGCCACCTTTCCCGAAAGTTCACCGAGTGGTGCTATGGGCCTGTCCG 1370
      | | | | | | | | | | | | | | | | | | | | | | | |
2199 TGCAGGCACCTGTCCAGGAAGTTCACCGAGTGGGCCTACGGGCCCCGTGCA 2248
      .
1371 GGTGTCGCTGTATGACCTGGCTTCTGTGGACAGCTGTGAGGAGAACTCAG 1420
      | | | | | | | | | | | | | | | | | | | | | | | |
2249 CTCCTCGCTGTACGACCTGTCTGCATCGACACCTGCGAGAAGAACTCGG 2298
      .
1421 TGCTGGAGATCATTCGCTTTCATTGCA...AGAGCCCGCACCGACACCGA 1467
      | | | | | | | | | | | | | | | | | | | | | | | |
2299 TGCTGGAGGTGATCGCCTACAGCAGCAGCGAGACCCCTAATCGCCACGAC 2348
      .
1468 ATGGTCGTTTTTGGAGCCCCTGAACAACTGCTGCAGGCGAAATGGGA... 1514
      | | | | | | | | | | | | | | | | | | | | | | | |
2349 ATGCTCTTGGTGGAGCCGCTGAACCGACTCCTGCAGGACAAGTGGGACAG 2398
      .
1515 TCTGCTCATCCCCAAGTTCTTCTTAACTTCCTGTGTAATCTGATCTACA 1564
      | | | | | | | | | | | | | | | | | | | | | | | |
2399 ATTCGTCAAGCGCATCTTCTACTTCAACTTCCTGGTCTACTGCCTGTACA 2448
      .
1565 TGTTTCATCTTCACCGCTGTTGCCTACCATCAGCCTACCCTGAAGAAGCAG 1614
      | | | | | | | | | | | | | | | | | | | | | | | |
2449 TGATCATCTTCACCATGGCTGCCTACTA...CAGGCCCGTGGATGGCTT 2494
      .
1615 GCCGCCCCCTCACCTGAAAGCGGAGGTTGGAACTCCATGCTGCTGACGGG 1664
      | | | | | | | | | | | | | | | | | | | | | | | |
2495 GCCTCCCTTTA..AGATGGAAAAAATTGGAGACTATTTCCGAGTTACTGG 2542
      .
1665 CCACATCCTTATCCTGCTAGGGGGGATCTACCTCCTCGTGGGCCAGCTGT 1714
      | | | | | | | | | | | | | | | | | | | | | | | |
2543 AGAGATCCTGTCTGTGTTAGGAGGAGTCTACTTCTTTTTCCGAGGGATTC 2592
      .
1715 GGTACTTCTGGCGGCGCCACGTGTTTCATCTGGATCTCGTTCATAGACAGC 1764
      | | | | | | | | | | | | | | | | | | | | | | | |
2593 AGTATTTCTGTCAGAGGCGGCCGTCGATGAAGACCCTGTTTGTGGACAGC 2642
```

Fig. 6D

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```
1765 TACTTTGAAATCCTCTTCTGTTCCAGGCCCTGCTCACAGTGGTGTCCCA 1814
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2643 TACAGTGAGATGCTTTTCTTTCTGCAGTCACTGTTTCATGCTGGCCACCGT 2692

1815 GGTGCTGTGTTTCTGGCCATCGAGTGGTACCTGCCCCCTGCTTGTGTCTG 1864
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2693 GGTGCTGTACTTCAGCCACCTCAAGGAGTATGTGGCTTCCATGGTATTCT 2742

1865 CGCTGGTGCTGGGCTGGCTGAACCTGCTTTACTATACACGTGGCTTCCAG 1914
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2743 CCCTGGCCTTGGGCTGGACCAACATGCTCTACTACACCGCGGGTTTCCAG 2792

1915 CACACAGGCATCTACAGTGTCTATGATCCAGAAGGTCATCCTGCGGGACCT 1964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2793 CAGATGGGCATCTATGCCGTCATGATAGAGAAGATGATCCTGAGAGACCT 2842

1965 GCTGCGCTTCCTTCTGATCTACTTAGTCTTCTTTTCGGCTTCGCTGTAG 2014
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2843 GTGCCGTTTCATGTTTGTCTACATCGTCTTCTTGTTCGGGTTTTCCACAG 2892

2015 CCCTGGTGAGCCTGAGCCAGGAGGCTTGGCGCCCCGAAGCTCCTACAGGC 2064
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2893 CGGTGGTGACGCTGATTGAAGACGGGAAGAATGACTCCCTGCCGTCTGAG 2942

2065 CCCAATGCCACAGAGTCAGTGCAGCCCATGGAGGGACAGGAGGACGAGGG 2114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2943 TCCA.....CGTCGCACAGGTGGCGGGGGCCTGCCTGCAGGCC 2980

2115 CAACGGGGCCCAGTACAGGGGTATCCTGGAAGCCTCCTTGGAGCTCTTCA 2164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2981 CCCCATAGCTCCTACAACAGCCTGTACTCCACCTGCCTGGAGCTGTTCA 3030

2165 AATTCACCATCGGCATGGGCGAGCTGGCCTTCCAGGAGCAGCTGCACTTC 2214
    ||| ||||| ||||| ||||| ||| ||| ||| ||| ||| ||| |||
3031 AGTTCACCATCGGCATGGGCGACCTGGAGTTCACTGAGAACTATGACTTC 3080

2215 CGCGGCATGGTGCTGCTGCTGCTGCTGGCCTACGTGCTGCTCACCTACAT 2264
    ||| ||| ||| ||| ||||| ||||| ||| ||| ||||| |||||
3081 AAGGCTGTCTTCATCATCCTGCTGCTGGCCTATGTAATTCTCACCTACAT 3130

2265 CCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCGTCAACAGTG 2314
    ||| ||||| ||||| ||||| ||||| ||| ||| ||||| |||||
3131 CCTCCTGCTCAACATGCTCATCGCCCTCATGGGTGAGACTGTCAACAAGA 3180
```

Fig. 6E

2315 TCGCCACTGACAGCTGGAGCATCTGGAAGCTGCAGARAGCCATCTCTGTG 2364
||| | | | | | | | | | | | | | | | |
3181 TCGCACAGGAGAGCAAGAACATCTGGAAGCTGCAGAGAGCCATCACCATC 3230
.
2365 CTGGAGATGGAGAATGGCTATTGGTGGTGCAGGAAGAAG...CAGCGGGC 2411
||| | | | | | | | | | | | | | | | |
3231 CTGGACACGGAGAAGAGCTTCCTTAAGTGCATGAGGAAGGCCCTTCCGCTC 3280
.
2412 AGGTGTGATGCTGACCGTTGGCACTAAGCCAGATGGCAGCCC GGATGAGC 2461
|| | | | | | | | | | | | | | | | | |
3281 AGGCAAGCTGCTGCAGGTGGGGTACACACCTGATGGCAAGGACGACTACC 3330
.
2462 GCTGGTGCTTCAGGGTGGAGGAGGTGAACTGGGCTTCATGGGAGCAGACG 2511
| | | | | | | | | | | | | | | | | |
3331 GGTGGTGCTTCAGGGTGGACGAGGTGAACTGGACCACCTGGAACACCAAC 3380
.
2512 CTGCCTACGCTGTGTGAGGACCCG...TCAGGGGCAGGTGTCCCTCGAAC 2558
|| | | | | | | | | | | | | | | | | |
3381 GTGGGCATCATCAACGAAGACCCGGGCAACTGTGAGGGCGTCAAGCGCAC 3430
.
2559 TCTCGAGAACCCTGTCTTG...GCTTCCCCCTCCAAGGAGGATGAGGAT 2604
|| | | | | | | | | | | | | | | | | |
3431 CCTGAGCTTCTCCCTGCGGTCAAGCAGAGTTTCAGGCAGACACTGGAAGA 3480
.
2605 GGTGCCTCTGAGGAAAACATATGTGCCCCGTCCAGCTCCTCCAGTCCAAC TG 2654
| | | | | | | | | | | | | | | | | |
3481 ACTTTGCCCTGGTCCCCCTTTTAAGAGAGGCAAGTGCTCGAGATAGGCAG 3530
.
2655 ATGGCCAGATGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTCCA 2704
|| ||| | | | | | | | | | | | | | |
3531 TCTGCTCAGCCCAGGAAGTTTATCTGCGACAGTTTTCAGGGTCTCTGAA 3580
.
2705 ACCACATCTGCTGGCTCTGGGGTCCCAGTGAATTCTGGTGGCAAATATAT 2754
||| | | | | | | | | | | | | | | |
3581 GCCA....GAGGACGCTGAGGTCTTCAAGAGTCCTGCCGCTTCCGGGGA 3625
.
2755 ATTTTCACTAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2804
| | | | | | | | | | | | | | | | | |
3626 GAAGTGAGGACGTCACGCAGACAGCACTGTCAACACTGGGGCCTTAGGAGA 3675
.
2805 AAAAA..... 2809
.
3676 CCCCCTTGCCACGGGGGGCTGCTGAGGGGAACACCAGTGCTCTGTGACGAG 3725

Fig. 6F

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CLUSTAL W (1.74) multiple sequence alignment

```

humanVR2      MTSPSSSPVFRLETLDGGQEDGSEADRGKLDGSGLPMPESQFQGEDRKFPQIRVNLNY
rat VR2      -----

humanVR2      RKG TGASQPDNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL
rat VR2      -----

humanVR2      MKAVLNLDGVMNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK
rat VR2      -----

humanVR2      LLVENGANVHARACGRFFQKGQGTCTFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQA
rat VR2      -----STHASALSLAACTKQWDVVTYLLENPHQPASLEA
                      .*****:*****:
                      .*****:*****:

humanVR2      TDSQGNTVLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL
rat VR2      TDSLGNFVLHALVMIADNSPENSALVIHMYDGLLQMGARLCPTVQLEEISNHQGLTPLKL
*** *****:***.*** ***** *****: * * .*****

humanVR2      AAKEGKIEIFRHILQREFSG-LSHL SRKFTWCYGPVRVSLYDLASVDSCEENS VLEIIA
rat VR2      AAKEGKIEIFRHILQREFSGPYQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSVLEIIA
*****:*****.*****:*****:*****

humanVR2      FHCKSPHRHRMVVLEPLNKLLOAKWDLIPKFLLNFLCNLIYMFIFTAVAYHQPTLKKQA
rat VR2      FHCKSPNRHRMVVLEPLNKLLOEKWDRLVSRFFNFACYLVMFIFTVAYHQPSLDQPA
*****:***** ***** *:..*: * *:*****.*****:..:

humanVR2      APHLKAEVGNMMLLTGHILILLGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQAL
rat VR2      IPSSKATFGESMLLLGHILILLGGIYLLVGQLWYFWRRLFIWISFMDSYFEILFLLQAL
* ** *:*****:*****:*****:*****:*****:*****

humanVR2      LTVVSQVLCFLAIEWYLP LLVSALVLGWLNL LYYTRGFQHIGIYSVMIQKVILRDLLRFL
rat VR2      LTVLSQVLRFMETEWYLP LLVLSVLGWLNL LYYTRGFQHTGIYSVMIQKVILRDLLRFL
***:**** *: ***** :*****:*****:*****:*****

humanVR2      LIYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDGNGAQYRGILEASLE
rat VR2      LVYLVFLFGFAVALVSLSREARSPKAPEDNNSTVTEQPTVGQEEEP--APYRSILDASLE
*:*****:*****:*** *:** *: * : * * *: * * * :*****

humanVR2      LFKFTIGMGELAFQEQQLHFRGMVLLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSI
rat VR2      LFKFTIGMGELAFQEQQLRFRGVLLLLLAYVLLTYVLLNMLIALMSETVNHVADNSWSI
*****:*****:*****:*****:***** ***** :****

humanVR2      WKLQKAISVLEMENGYWWCR-KKQ RAGVMLTVGTPDGSPDERWCFRVEEVN WASWEQTL
rat VR2      WKLQKAISVLEMENGYWWCRRKKHREGRL LKVGTRGDGTPDERWCFRVEEVNKA AWEKTL
*****:***** ***** *: * *: * *: * *:*****:*****:*****

humanVR2      PTLCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLQSN
rat VR2      PTLSEDPSGPGITGNKNPTSK-PGK---NSASEEDHLPQLVQSP
***.*****:..: :***. * * :.*****:..:*****

```

Fig. 7

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GAP of: ratvr2.pep check: 9190 from: 1 to: 554

ratVR2 Flrxb147g11

to: humanvr2.pep check: 5746 from: 1 to: 764

humanVR2 Flh21e11

Symbol comparison table: /usr/local/gog_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	2182	Length:	766
Ratio:	3.939	Gaps:	4
Percent Similarity:	81.703	Percent Identity:	79.167

Match display thresholds for the alignment(s) :
| = IDENTITY
: = 2
. = 1

ratvr2.pep x humanvr2.pep

```

      .           .           .           .           .
1  ....STHASALSLAACTKQWDVVITYLLENPHQPASLEATDSLGN TVLH 44
      |||||||
201 GQGTCTFYFGELPLSLAACTKQWDVVSYLENPHQPASLQATDSQGN TVLH 250
      .           .           .           .           .
45 ALVMIADNSPENSALVIHMYDGLLQMGARLCPTVQLEEISNHQGLT PLKL 94
      |||||.||| || ||| ||||||| ||||||| |||||:| | |||||
251 ALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLT PLKL 300
      .           .           .           .           .
95 AAKEGKIEIFRHILQREFSGPYQPLSRKFTEWCYGPVRVSLYDLSSV DSW 144
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||.|||
301 AAKEGKIEIFRHILQREFSG.LSHLSRKFTWCYGPVRVSLYDLASV DSC 349
      .           .           .           .           .
145 EKNSVLEIIAFHCKSPNRHRMVVLEPLNKLLOEKWDRLVSRPFFNF ACYL 194
      |.||||| |||||||.||||| ||||||| |||||:|:| |||||
350 EENS VLEIIAFHCKSPHRHRMVVLEPLNKLLOAKWDLLIPKFFLNFL CNL 399
      .           .           .           .           .
195 VYMFIFTVVAYHQPSLDQPAIPSSKATFGESMLLLGHILILLGGIY LLLG 244
      :||||| |||||||. | . | | | | ||||| ||||||| |||||.
400 IYMFIFTAVAYHQPTLKKQAAPHLKAEVGNSMLLTGHILILLGGIY LLVG 449

```

Fig. 8A

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```

245 QLWYFWRRRLFIWISFMDSYFEILFLLQALLTVLSQVLRFMETEWYLP LL 294
    ||||| . ||||| . ||||| ||||| . ||||| : |||||
450 QLWYFWRRHVFIWISFIDSYFEILFLFQALLTVVSQVLCFLAIEWYLP LL 499
    || . ||||| ||||| ||||| ||||| ||||| ||||| : |||||
295 VLSLVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLVYLVFLFGF 344
    | . ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
500 VSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGF 549
    || . ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
345 AVALVSLSREARSPKAPEDNNSTVTEQPTVGQEEE . . PAPYRSILDASLE 392
    ||||| . || . || . || . || ||| : | | | | : |||||
550 AVALVSLSQEAWRPEAPTGNATESVQPMEGQEDEGNGAQYRGILEASLE 599
    || . ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
393 LFKFTIGMGELAFQEQLRFRGVVLLLLLAYVLLTYVLLLNMLIALMSETV 442
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
600 LFKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLNMLIALMSETV 649
    || . ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
443 NHVADNSWSIWKLQKAISVLEMENGYWWCRRKKHREGRLKVGTRGDGTP 492
    | | | . ||||| ||||| ||||| ||||| ||||| ||||| : | | | : | | . |
650 NSVATDSWSIWKLQKAISVLEMENGYWWC . RKKQRAGVMLTVGTPDGSP 698
    || . ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
493 DERWCFRVEEVNWAWEKTLPTLSEDPSGPGITGNKKNPT . . . . SKPGKN 538
    ||||| ||||| ||||| . || . ||||| ||||| ||||| : . || . . . .
699 DERWCFRVEEVNWAWEQTLPTLCEDPGAGVPRTLENPVLASPPKEDED 748
    ||||| . . . . .
539 SASEEDHLP LQVLQSP 554
    |||| . . . . .
749 GASEENYVPVQLQSN 764
```

Fig. 8B

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GAP of: humanvr1.seq check: 4554 from: 1 to: 3909

humanVR1 Fbh18547pat - Import - complete

to: ratvr1.seq check: 7921 from: 1 to: 2847

ratVR1.seq AF029310 in GenBank

Symbol comparison table:
/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	22717	Length:	3914
Ratio:	7.979	Gaps:	10
Percent Similarity:	82.125	Percent Identity:	82.125

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

humanvr1 . seq x ratvr1 . seq

```

      .
      .
      .
1001 CCAGGCCGTAGATGCTCCCCGCCGGTCAGTCACTTAGTCGTCAGATCGCC 1050
      |||||
      1 .....CAGCTCCAAGGCACTTGCTCC 21
      .
      .
1051 CGTCCTGGTATCACAGTGCTTCTGTTCAGGTTGCACACTGGGCCACAGAG 1100
      |||||
      22 ATTTGGGGTGTGCCTGCACCT...AGCTGGTTGCAAATTGGGCCACAGAG 68
      .
      .
1101 GATCCAGCAAGGATGAAGAAATGGAGCAGCACAGACTTGGGGACAGCTGC 1150
      |||||
      69 GATCTGGAAGGATGGAACAACGGGCTAGCTTAGACTCAGAGGAGTCTGA 118
      .
      .
1151 GGACCCACTCCAAAAGGACACCTGCCCAGACCCCCTGGATGGAGACCCTA 1200
      |||||
      119 GTCCCCACCCAAGAGAACTCCTGCCTGGACCCTCCAGACAGAGACCCTA 168

```

Fig. 9A

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```
1201 ACTCCAGGCCACCTCCAGCCAAGCCCCAGCTCCCCACGGCCAAGAGCCGC 1250
    ||| || ||||| ||||| ||||| ||| ||| ||| |||
169 ACTGCAAGCCACCTCCAGTCAAGCCCCACATCTTCACTACCAGGAGTCGT 218
    .
1251 ACCCGGCTCTTTGGGAAGGGTGACTCGGAGGAGGCTTTCCCGGTGGATTG 1300
    ||||| ||||| ||||| ||||| ||||| ||| ||| ||| |||
219 ACCCGGCTTTTGGGAAGGGTGACTCGGAGGAGGCCTCTCCCTGGACTG 268
    .
1301 CCCCCACGAGGAAGGTGAGTTGGACTCCTGCCCCACCATCACAGTCAGCC 1350
    ||| ||| ||||| ||||| ||||| ||||| |||||
269 CCCTTATGAGGAAGCGGGCTGGCTTCCTGCCCTATCATCACTGTCAGCT 318
    .
1351 CTGTTATCACCATCCAGAGGCCAGGAGACGGCCCCACGGTGCCAGGCTG 1400
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
319 CTGTTCTAACTATCCAGAGGCCTGGGGATGGACCTGCCAGTGTGAGGCCG 368
    .
1401 CTGTCCCAGGACTCTGTGCGCCAGCACCGAGAAGACCCTCAGGCTCTA 1450
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
369 TCATCCCAGGACTCCGTCTCCGCTGG...TGAGAAGCCCCGAGGCTCTA 415
    .
1451 TGATCGCAGGAGTATCTTTGAAGCCGTTGCTCAGAATAACTGCCAGGATC 1500
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
416 TGATCGCAGGAGCATCTTCGATGCTGTGGCTCAGAGTAACTGCCAGGAGC 465
    .
1501 TGGAGAGCCTGCTGCTCTTCCTGCAGAAGAGCAAGAAGCACCTCACAGAC 1550
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
466 TGGAGAGCCTGCTGCCCTTCCTGCAGAGGAGCAAGAAGCGCCTGACTGAC 515
    .
1551 AACGAGTTCAAAGACCCTGAGACAGGGAAGACCTGTCTGCTGAAAGCCAT 1600
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
516 AGCGAGTTCAAAGACCCAGAGACAGGAAAGACCTGTCTGCTAAAAGCCAT 565
    .
1601 GCTCAACCTGCACGACGGACAGAACACCACCATCCCCCTGCTCCTGGAGA 1650
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
566 GCTCAATCTGCACAATGGGCAGAATGACACCATCGCTCTGCTCCTGGACG 615
    .
1651 TCGCGCGGCAAACGGACAGCCTGAAGGAGCTTGTCAACGCCAGCTACACG 1700
    ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
616 TTGCCCGGAAGACAGACAGCCTGAAGCAGTTTGTCAATGCCAGCTACACA 665
    .
1701 GACAGCTACTACAAGGGCCAGACAGCACTGCACATCGCCATCGAGAGACG 1750
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
666 GACAGCTACTACAAGGGCCAGACAGCACTGCACATTGCCATTGAACGGCG 715
```

Fig. 9B

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```
1751 CAACATGGCCCTGGTGACCCTCCTGGTGGAGAACGGAGCAGACGTCCAGG 1800
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
716 GAACATGACGCTGGTGACCCTCTGGTGGAGAATGGAGCAGATGTCCAGG 765

1801 CTGCGGCCCATGGGGACTTCTTTAAGAAAACCAAAGGGCGGCCTGGATTG 1850
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
766 CTGCGGCTAACGGGGACTTCTTCAAGAAAACCAAAGGGAGGCCTGGCTTC 815

1851 TACTTCGGTGAAGTGCCCTGTCCCTGGCCGCGTGCACCAACCAGCTGGG 1900
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
816 TACTTTGGTGAGCTGCCCTGTCCCTGGCTGCGTGCACCAACCAGCTGGC 865

1901 CATCGTGAAGTTCCTGCTGCAGAACTCCTGGCAGACGGCCGACATCAGCG 1950
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
866 CATTGTGAAGTTCCTGCTGCAGAACTCCTGGCAGCCTGCAGACATCAGCG 915

1951 CCAGGGACTCGGTGGGCAACACGGTGCTGCACGCCCTGGTGGAGGTGGCC 2000
      || ||||| ||||| ||||| ||||| ||||| ||||| |||||
916 CCCGGGACTCAGTGGGCAACACGGTGCTTCATGCCCTGGTGGAGGTGGCA 965

2001 GACAACACGGCCGACAACACGAAGTTTGTGACGAGCATGTACAATGAGAT 2050
      || ||||| | ||||| ||||| ||||| ||||| ||||| |||||
966 GATAACACAGTTGACAACACCAAGTTCGTGACAAGCATGTACAACGAGAT 1015

2051 TCTGATGCTGGGGGCCAAACTGCACCCGACGCTGAAGCTGGAGGAGCTCA 2100
      |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1016 CTTGATCCTGGGGGCCAAACTCCACCCACGCTGAAGCTGGAAGAGATCA 1065

2101 CCAACAAGAAGGGAATGACGCCGCTGGCTCTGGCAGCTGGGACCGGGAAG 2150
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1066 CCAACAGGAAGGGGCTCAGCCACTGGCTCTGGCTGCTAGCAGTGGGAAG 1115

2151 ATCGGGGTCTTGGCCTATATTCTCCAGCGGGAGATCCAGGAGCCCGAGTG 2200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1116 ATCGGGGTCTTGGCCTACATTCTCCAGAGGGAGATCCATGAACCCGAGTG 1165

2201 CAGGCACCTGTCCAGGAAGTTCACCGAGTGGGCCTACGGGCCCCGTGCACT 2250
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1166 CCGACACCTATCCAGGAAGTTCACCGAATGGGCCTATGGGCCAGTGCACT 1215

2251 CCTCGCTGTACGACCTGTCCTGCATCGACACCTGCGAGAAGAACTCGGTG 2300
      |||| || || ||||| ||||| ||||| ||||| ||||| |||||
1216 CCTCCCTTTATGACCTGTCCTGCATTGACACCTGTGAAAAGAACTCGGTT 1265
```

Fig. 9C

Fig. 9D

Fig. 9E

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```
3398 AGACCCGGGCAACTGTGAGGGCGTCAAGCGCACCTGAGCTTCTCCCTGC 3447
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2363 GGACCCAGGCAACTGTGAGGGCGTCAAGCGCACCTGAGCTTCTCCCTGA 2412
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3448 GGTCAAGCAGAGTTTCAGGCAGACACTGGAAGAACTTTGCCCTGGTCCCC 3497
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2413 GGTCAAGCCGAGTTTCAGGGAGAACTGGAAGAACTTTGCCCTGGTTCCT 2462
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3498 CTTTTAAGAGAGGCAAGTGCTCGAGATAGGCAGTCTGCTCAGCCCGAGGA 3547
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2463 CTTCTGAGGGATGCAAGCACTCGAGATAGACATGCCACCCAGCAGGAAGA 2512
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3548 AGTTTATCTGCGACAGTTTTCAGGGTCTCTGAAGCCAGAGGACGCTGAGG 3597
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2513 AGTTCAACTGAAGCATTATACGGGATCCCTTAAGCCAGAGGATGCTGAGG 2562
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3598 TCTTCAAGAGTCTGCGCGCTTCCGGGGAGAAAGTGA.GGACGTCACGCAGA 3646
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2563 TTTTCAAGGATTCCATGGTCCCAGGGGAGAAATAATGGACACTATGCAGG 2612
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3647 CAGCACTGTCAAACTGAGGCTTAGGAGACCCCGTTGCCACGGGGGGCTG 3696
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2613 GATCAATG.....CGGGGTCTTTGGGTGGTCTG 2640
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3697 CTGAGGGGAACACCAAGTGCTCTGTGTCAGCAGCCTGGCCTGGTCTGTGCCTGC 3746
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2641 CTTAGGGGAAC.CAGCAGGGTTGACGTTATCTGGGTCCACTCTGTGCCTGC 2689
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3747 CCA.GCATGTTCCCAAATCTGTGCTGGACAAGCTGTGGGAAGCGTTCTTG 3795
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2690 CTAGGCACATTCTTAGGACTTCGGCGGGCCTGCTGTGGGAA.CTGGGAGG 2738
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3796 GAAGCATGGGGAGTGATGTACATCCAACCGTCACTGTCCCAAGTGAATC 3845
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2739 TGTGTGGGAATTGAGATGTGTATCCAACCATGA...TCTCCAAACATTTG 2785
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3846 TCCTAACAGACTTTCAGGTTTTTACTCACTTTACTAAAAAAAAAAAAAAAA 3895
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2786 GCTTTCAACTCTTTATGGACTTTATTAAACAGAGTGAATGGCAAATCTCT 2835
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3896 AGGGCGGCCGCTTA 3909
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2836 ACTTGGACACAT.. 2847
```

Fig. 9F

GAP of: humanvr1.pep check: 6877 from: 1 to: 839

to: ratvr1.pep check: 5764 from: 1 to: 838

Symbol comparison table:

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003

Percent Similarity: 89.247 Percent Identity: 86.022

| = IDENTITY

$$\vdots = 2$$

. = 1

1 MKKWSSTD LGTAADPLQKDTCPDPLDGD P NSRPPPAKPQLPTAKSRTL F 50

| . . . | | . | | . . . | . | . | | . : | | : | | |

1 MEQRASLDSEESPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSRTL 50

51 GKGDSEEAFPVDCPHEEGELDSCTITVSPVITIQRPGDGPTGARLLSQD 100

$$\frac{1}{2} \left(\frac{1}{2} + \frac{1}{2} \right) = \frac{1}{2}$$

101 SVAASTEKTLRLYDRRSIFEAVAQNNCQDLESLLLFLQSKKHLTDNEFK 150

||. || |||||: ||. ||: |||: |||: |||.

101 SVSAG.EKPPRLYDRRSIFDAVAQSNQLESLLPFLQSKKRLTDSEFK 149

151 DPETGKTCLLKAMLNLDGONTTIPLLLEIAROTDSLKELVNASYTDSYY 200

||||| . ||| :: . ||| :

150 DPETGKTCLLKAMLNLENGONDTIALLLDVARKTDSLKQFVNASYTDSYY 199

201 KGOTALHIAIERRNMAVLTLLVENGADVOAAAHGDFFKTKGRPGFYFGE 250

.....

200 KGOTALHIAIERRNMTLVTLVENGADVQAAANGDFFKKTGKRPGFYFGE 249

Fig. 10A

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```

251 LPLSLAACTNQLGIVKFLQLNSWQTADISARDSVGNTVLHALVEVADNTA 300
|||||
250 LPLSLAACTNQLAIVKFLQLNSWQPADISARDSVGNTVLHALVEVADNTV 299
|||||

301 DNTKFVTSMYNEILMLGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVL 350
|||||
300 DNTKFVTSMYNEILILGAKLHPTLKLEELTNRKGLTPLALAASSGKIGVL 349
|||||

351 AYILQREIQEPECRHLSRKFTWAYGPHSSLYDLSCIDTCEKNSVLEVI 400
|||||
350 AYILQREIHEPECRHLSRKFTWAYGPHSSLYDLSCIDTCEKNSVLEVI 399
|||||

401 AYSSSETPNRHDMLLVEPLNRLLODKWDRFVKRIFYFNFLVYCLYMIIFT 450
|||||
400 AYSSSETPNRHDMLLVEPLNRLLODKWDRFVKRIFYFNFFVYCLYMIIFT 449
|||||

451 MAAYYRPVDGLPPFKMEK.IGDYFRVTGEILSVLGGVYFFFRGIQYFLQR 499
|||||
450 AAAYYRPVEGLPPYKLNKTVGDYFRVTGEILSVSGGVYFFFRGIQYFLQR 499
|||||

500 RPSMKTLFVDSYSEMLFFLQSLFMLATVVLYFSLKEYVASMVFSALGW 549
|||||
500 RPSLKSFLVDSYSEILFFVQSLFMLVSVVLYFSQRKEYVASMVFSAMGW 549
|||||

550 TNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVYIVFLFGFSTAVVTLI 599
|||||
550 TNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLI 599
|||||

600 EDGKNDSLPESTSHRWGPACRPPDSSYNLSYSTCLELFKFTIGMGDLE 649
|||||
600 EDGKNNSLPESTPHKCRGSACK.PGNSYNLSYSTCLELFKFTIGMGDLE 648
|||||

650 FTENYDFKAVFIILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWK 699
|||||
649 FTENYDFKAVFIILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWK 698
|||||

700 LQRAITILDTEKSFLKCMRKAFRSGKLLQVGYPDGDYRWCFRVDEVN 749
|||||
699 LQRAITILDTEKSFLKCMRKAFRSGKLLQVGFTPDGDYRWCFRVDEVN 748
|||||

750 WTTWNTNVGIINEDPGNCEGVKRTLSFSLRSSRVSGRHWKNFALVPLLRE 799
|||||
749 WTTWNTNVGIINEDPGNCEGVKRTLSFSLRSGRVSGRNWKNFALVPLLRD 798
|||||

800 ASARDRQSAQPEEVYLRQFSGSLKPEDA EVFKSPAASGEK 839
|||||
799 ASTRDRHATQEEVQLKHYTGSLKPEDA EVFKDSMVPGEK 838
|||||

```

Fig. 10B

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CLUSTAL W (1.74) multiple sequence alignment

```

humanVR2.alt -----
human VR2      MTSPSSSPVFRLETLDGGQEDGSEADRGKLDGSGLPMPESQFQGEDRKFPQIRVNLNY

humanVR2.alt -----
human VR2      RKG TGASQPDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL

humanVR2.alt -----
human VR2      MKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK

humanVR2.alt -----GRFFQKQGQTCFYFGELPLSLAACTKQWDVVSYLENPHQPASLQA
human VR2      LLVENGANVHARACGRFFQKQGQTCFYFGELPLSLAACTKQWDVVSYLENPHQPASLQA
                      *****

humanVR2.alt TDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL
human VR2      TDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL
                      *****

humanVR2.alt AAKEGKIEIFRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVEIIAF
human VR2      AAKEGKIEIFRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVEIIAF
                      *****

humanVR2.alt HCKSPHRHRMVLEPLNKLLOAKWDLLIPKFFDNFLCNLIYMFIFTAVAYHQPTLKKQAA
human VR2      HCKSPHRHRMVLEPLNKLLOAKWDLLIPKFFDNFLCNLIYMFIFTAVAYHQPTLKKQAA
                      *****

humanVR2.alt PHLKAEVGNSMLLTGHILILLGGIYLLVGQLWYFWRHRVFIWISFIDSYFEILFLFQALL
human VR2      PHLKAEVGNSMLLTGHYLILLGGIYLLVGQLWYFWRHRVFIWISFIDSYFEILFLFQALL
                      *****

humanVR2.alt TVVSQVLCFLAIEWYLPLLVSALVLGWLNLLEYTRGFQHTGIYSVMIQ-----
human VR2      TVVSQVLCFLAIEWYLPLLVSALVLGWLNLLEYTRGFQHTGIYSVMIQKVILRDLLRFL
                      *****

humanVR2.alt -----
human VR2      IYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLEL

humanVR2.alt -----
human VR2      FKFTIGMGELAFQEQHLFRGMVLLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW

humanVR2.alt --KKAISVLEMENGYWWCRKKQRAGVMLTVGTPDGSPDERWCFRVEEVNWSWEQTLPT
human VR2      KLQKAI SVLEMENGYWWCRKKQRAGVMLTVGTPDGSPDERWCFRVEEVNWSWEQTLPT
                      : *****

humanVR2.alt LCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN
human VR2      LCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN
                      *****

```

Fig. 11

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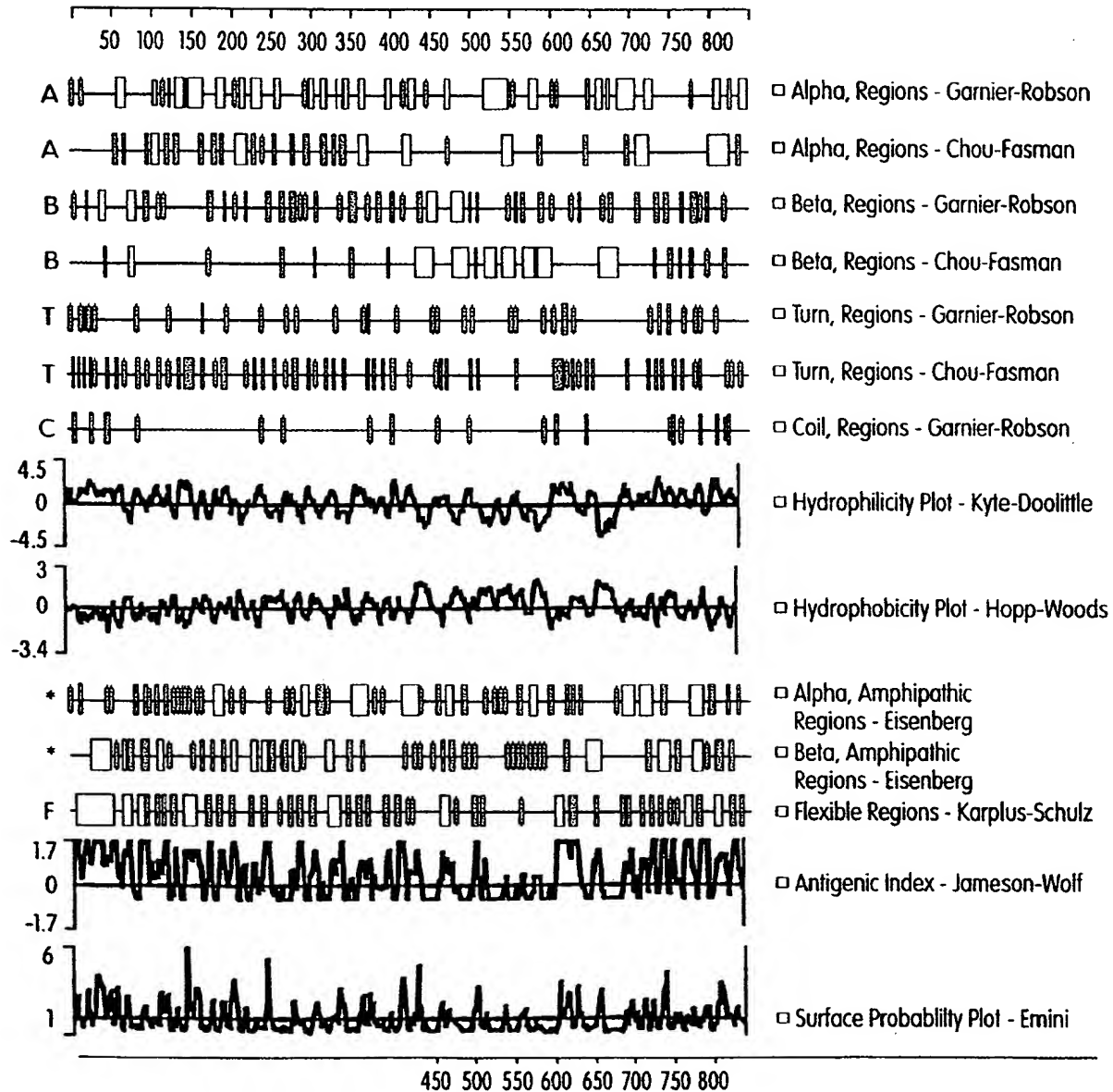


Fig. 12

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Protein Family / Domain Matches, HMMer version 2

Searching for complete domains

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

Copyright (C) 1992-1998 Washington University School of Medicine

HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam4.2/Pfam
Sequence file: /usr/ns-home/docs/seqanal/orfanal/oa-script 18670 seq

Query: hVR-1

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
ank	Ank repeat	51.5	1.9e-11	3

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
ank	1/3	201	233 ..	1	33 []	34.4	2.6e-06
ank	2/3	248	283 ..	1	33 []	13.2	2
ank	3/3	333	361 ..	1	33 []	3.4	26

Alignments of top-scoring domains:

ank: domain 1 of 3, from 201 to 233: score 34.4, E = 2.6e-06

->nGnTPLHLAarygnvevvklLLLehGAdvnartk<-
+G+T+LH+A + nt +v lL+e+GAdv a+

hVR-1 201 KGQTALHIAIERRNMALVTLLVENGADVQAAAH 233

ank: domain 2 of 3, from 248 to 283: score 13.2, E = 2

->nGnTPLHLAarygnvevvklLLLe...hGAdvnartk<-
G PL lAa ++++ +vk+LL+++ + Ad+ ar+

hVR-1 248 FGELPLSLAACTNQLGIVKFLQLQswQTADISARDS 283

ank: domain 3 of 3, from 333 to 361: score 3.4, E = 26

->nGnTPLHLAarygnvevvklLLLehGAdvnartk<-
+G TPL lAa +g++ v ++ L+ ++

hVR-1 333 KGMTPLALAAAGTGKIGVLAYILQ----REIQEP 361

Fig. 13

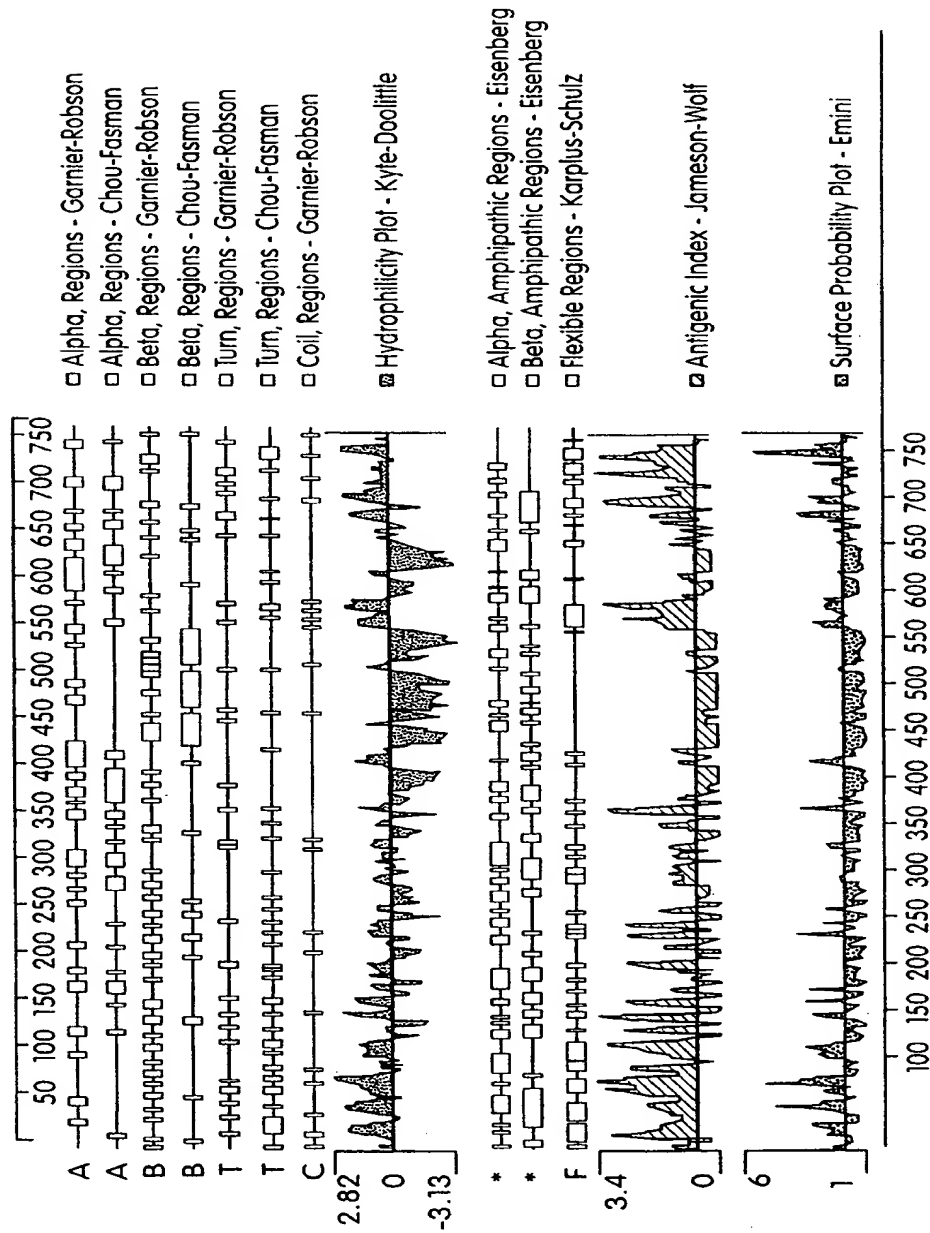


Fig. 14

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Protein Family / Domain Matches, HMMer version 2

Searching for complete domains

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

Copyright (C) 1992-1998 Washington University School of Medicine

HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam4.2/Pfam

Sequence file: /tmp/orfanal.5/g.aa

Query: Flh21e11

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
ank	PF00023 Ank repeat	53.7	4e-12	3

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
ank	1/3	162	194 ..	1	33 []	38.3	1.7e-07
ank	2/3	208	243 ..	1	33 []	6.4	4.3
ank	3/3	293	328 ..	1	33 []	8.8	2.1

Alignments of top-scoring domains:

ank: domain 1 of 3, from 162 to 194: score 38.3, E = 1.7e-07

->nGnTPLHLAarygnvevklLLehGAdvnartk<-

+G+++LH+A ++ ++++vklL+e+GA+v+ar

Flh21e11 162 RGHSALHIAIEKRSLQCVKLLVENGANVHARAC 194

ank: domain 2 of 3, from 208 to 243: score 6.4, E = 4.3

->nGnTPLHLAarygnvavvklLLe...hGAdvnartk<-

G PL lAa + +++vv +LLe++++ A+ a++

Flh21e11 208 FGELPLSLAACTKQWDVVSYGLEnphQPASLQATDS 243

ank: domain 3 of 3, from 293 to 328: score 8.8, E = 2.1

->nGnTPLHLAarygnvevklLLe...hGAdvnartk<<-

+ +TPL lAa++g++e+ + L+++ G + +r

Flh21e11 293 QDLTPLKLAKEQKLEIFRHILQrafSGLSHLSRK 328

Fig. 15

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>hvr2.altFL (full-length predicted)
MTSPSSSPVFRLETLGGQEDGSEADRGKLDFGSLPPMESQFQGEDRKFAPIRVNLNY
RKGTGASQPDNRFDRDLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL
MKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK
LLVENGANVHARACGRFFQKGQGTCTFYFGELPLSLAACTKQNDVVSYLENPHQPASLQATSQGNTVLHALVM
ISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAKEGKIEIFRHIL
QREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAFHCKSPHRHRMVVLE
PLNKLQAKWDLLIPKFFLNFLCNLIYMFIFTAVAYHQPTLKKQAAPHLKAEVGNSMLLT
GHILILLGGIYLLVGQLWYFWRHVFIIWISFIDSFYFEILFLFQALLTVVSQVLCFLAIEW
YLPLLVSAVLGWLNLYYTRGFQHTGIYSVMIQKKAISVLEMENGYWCCRKKQRAGVML
TVGTKPDGSPDERWCFRVEEVNWAWEQTLPTLCEDPGAGVPRTLNPNVLASPPKDED
GASEENYVPVQLLSN

Fig. 16

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CLUSTAL W (1.74) multiple sequence alignment

```
humanVR2      MTSPSSSPVFRLETLDGGQEDGSEADRGKLDGSGSLPPMESQFQGEDRKFPQIRVNLNY
hVR2.altfL    MTSPSSSPVFRLETLDGGQEDGSEADRGKLDGSGSLPPMESQFQGEDRKFPQIRVNLNY
*****

humanVR2      RKG TGASQPDNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL
hVR2.altfL    RKG TGASQPDNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL
*****

humanVR2      MKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRS LQCVK
hVR2.altfL    MKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRS LQCVK
*****

humanVR2      LLVENGANVHARACGRFFQKGQGTCTFYFGELPLSLAACTKQWDVVS YLLENPHQPASLQA
hVR2.altfL    LLVENGANVHARACGRFFQKGQGTCTFYFGELPLSLAACTKQWDVVS YLLENPHQPASLQA
*****

humanVR2      TDSQGNTVLHALVMISDN SAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL
hVR2.altfL    TDSQGNTVLHALVMISDN SAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL
*****

humanVR2      AAKEGKIEIFRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEI IAF
hVR2.altfL    AAKEGKIEIFRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEI IAF
*****

humanVR2      HCKSPHRHRMVVLEPLNKL LQAKWDLLIPKFFLNFLCNLIYMFIFTAVAYHQPTLKKQAA
hVR2.altfL    HCKSPHRHRMVVLEPLNKL LQAKWDLLIPKFFLNFLCNLIYMFIFTAVAYHQPTLKKQAA
*****

humanVR2      PHLKAEVGNSMLLTGHI LILLGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQALL
hVR2.altfL    PHLKAEVGNSMLLTGHI LILLGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQALL
*****

humanVR2      TVVSQVLCFLAIEWYLP LLVSALVLGWLNL LYYTRGFQHTGIYSVMIQKVILRDLLRFL
hVR2.altfL    TVVSQVLCFLAIEWYLP LLVSALVLGWLNL LYYTRGFQHTGIYSVMIQK-----
*****

humanVR2      IYLVFLFGFAVALVSL SQAWRPEAPTGNATESVQPMEGQEDGNGAQYRGILEASLEL
hVR2.altfL    -----

humanVR2      FKFTIGMGE LAFQEQ LHFGRGMVLLLLL AYVLLTYILLNMLIALMSETVNSVATDSWSIW
hVR2.altfL    -----

humanVR2      KLQKAISVLEMENGYW WCRKKQRAGVMLTVGTPDGSPDERWCFRVEEVN WASWEQTLPT
hVR2.altfL    ---KAISVLEMENGYW WCRKKQRAGVMLTVGTPDGSPDERWCFRVEEVN WASWEQTLPT
*****

humanVR2      LCEDPSGAGVPRTLEN PVLASPPKEDEGASEENYVPVQLLQSN
hVR2.altfL    LCEDPSGAGVPRTLEN PVLASPPKEDEGASEENYVPVQLLQSN
*****
```

Fig. 17